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W P E L H (TW)  
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Release 2.1D John F. Collins, Biocomputing Research Unit.  
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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Thu Feb 6 12:26:06 1997; MasPar time 21.99 Seconds  
632.952 Million cell updates/sec  
Tabular output not generated.

File: >US-08-468-011-2  
Description: (1-541) from US08468011.pep  
Accession: 4132  
Sequence: 1 MAWLGLASLHWGWLMLGSLC.....DDLMEKPSRPMESNPDTEG 541

Scoring table: PAM 150  
Gap 11  
Searched: 82182 seqs, 25727515 residues  
Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: pir48  
1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4  
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc  
14:unrev

Statistics: Mean 48.841; Variance 115.276; scale 0.424  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Description	Pred. No.
1	3721	90.1	parathyroid hormone	0.00e+00
2	2051	49.6	parathyroid hormone	0.00e+00
3	1966	47.6	parathyroid hormone	0.00e+00
4	1943	47.0	parathyroid hormone	0.00e+00
5	1942	47.0	parathyroid hormone	0.00e+00
6	1931	46.7	parathyroid hormone	0.00e+00
7	1026	24.8	parathyroid hormone	1.30e-150
8	1003	24.3	vasoactive intestina	1.30e-150
9	990	24.0	vasoactive intestina	2.72e-144
10	983	23.8	vasoactive intestina	4.59e-143
11	975	23.6	secretin receptor	1.16e-141
12	964	23.3	secretin receptor	9.80e-140
13	907	22.0	PACAP receptor subty	9.11e-130
14	900	21.8	vasoactive intestina	1.52e-128
15	877	21.2	vasoactive intestina	1.56e-124
16	863	20.9	glucagon-like peptid	4.28e-122
17	845	20.5	glucagon receptor pr	5.84e-119
18	843	20.4	GLP-1 receptor	1.29e-118
19	825	20.0	GLP-1 receptor - hum	1.74e-115
20	818	19.8	glucagon-like peptid	2.85e-114
21	816	19.7	glucagon receptor	6.35e-114

22	807	19.5	462 12	JC2462	gastric inhibitory p	2.31e-112
23	793	19.2	467 12	JN0616	pituitary adenylate	6.18e-110
24	782	18.9	490 11	S34486	calcitonin receptor	4.97e-108
25	780	18.9	525 11	JN0902	pituitary adenylate	1.10e-107
26	762	18.4	423 11	A45367	growth hormone-relea	1.43e-104
27	757	18.3	423 11	A45363	growth hormone-relea	1.04e-103
28	754	18.2	516 12	S33747	calcitonin receptor	3.45e-103
29	737	17.8	474 11	S44209	calcitonin receptor	2.96e-100
30	711	17.2	423 12	S29753	growth hormone-relea	8.89e-96
31	704	17.0	479 12	S33746	calcitonin receptor	1.42e-94
32	653	15.8	482 12	A39285	calcitonin receptor	7.88e-86
33	644	15.6	461 11	JC2477	calcitonin receptor	2.72e-84
34	595	14.4	415 11	S39534	corticotropin-relea	5.98e-76
35	591	14.3	415 12	S39535	corticotropin-relea	2.85e-75
36	584	14.1	430 12	A56726	corticotropin recep	4.38e-74
37	542	13.1	494 14	S39063	pituitary adenyl c	5.42e-67
38	538	13.0	495 12	S36114	pituitary adenylate	2.55e-66
39	538	13.0	495 14	S39061	pituitary adenyl c	2.55e-66
40	538	13.0	495 12	A48204	pituitary adenylate	2.55e-66
41	538	13.0	523 14	S39060	pituitary adenyl c	2.55e-66
42	535	12.9	381 12	S33449	pituitary adenylate	8.15e-66
43	533	12.9	513 14	A47631	pituitary adenylate	1.77e-65
44	456	11.0	464 12	S29754	growth hormone-relea	1.23e-52
45	270	6.5	206 10	S23242	hypothetical protein	7.35e-23

ALIGNMENTS

RESULT 1  
ENTRY A57519 #type complete  
TITLE parathyroid hormone receptor 2 precursor - human  
ALTERNATE\_NAMES PTH2 receptor  
ORGANISM #formal name Homo sapiens #common name man  
DATE 08-Dec-1995 #sequence\_revision 08-Dec-1995 #text\_change  
ACCESSIONS A57519  
REFERENCE A57519  
#authors Usdin, T.B.; Gruber, C.; Bonner, T.I.  
#journal J. Biol. Chem. (1995) 270:15455-15458  
#title Identification and functional expression of a receptor  
selectively recognizing parathyroid hormone, the PTH2  
receptor.  
#accession A57519  
#status preliminary  
#molecule\_type mRNA  
#residues 1-550 #label USD  
#cross-references GB:025128  
#note nucleotide sequence not given  
KEYWORDS hormone receptor  
SUMMARY #length 550 #molecular-weight 62235 #checksum 2724

6/30/95

Query Match					90.1%; Score 3721; DB 11; Length 550;
Best Local Similarity					91.5%; Pred. No. 0.00e+00;
Matches					496; Conservative 18; Mismatches 26; Indels 2; Gaps 2;
Db	1	magigaslhvqwlmgscllaragldsgdtit	eeqivlvkavqcelnitaqlqege	60	
Qy	1	MAWLGLASLHWGWLMLGSLC	LDSDGTITIEEQIVLVKAKVQCELNIT	60	
Db	61	gncfpewdglcwpgrgtvgkisavpcpp	pyiydfnhkgvafrcncpntgdfmsh	120	
Qy	61	GNCFPEWDGLICWPGRTVGKISAVPCPP	YIYDFNKHGVAFRCNPNGTWDFMHS	120	
Db	121	nysdclrfiqpdislgkqef	ferlymvtvgysifsgslavallig	180	
Qy	121	NYSDCLRFQPDISTIGQEF	ERLYVMYTVGYSISFGSLAVAILI	180	
Db	181	mhlvsvfmlratsifvdkrvv	hahgveleslmqddpqnscatsv	240	
Qy	181	MHLVSVFMLRATISFVKDRVV	HAHIGVELESIMQDDPQNSIEAT	240	
Db	241	vmfiyflatnywllveqly	lhnlfvaffsdtkylgfligwgf	300	
Qy	241	VMFIYFLATNYWLLVEQLY	LHNLFFVAFSDTKYLGFLIGWGF	300	

QY	241	VMIYIFLATNYWIIWEGVLYLHNLIFVAFESTKYLIMGFILIGWGFPAAFVAAVAVARAT	300
Db	301	ladarcwelsagdkwiygapilaaiglnfiilntvrvtlatkiwethnavghdtrkqyrk	360
QY	301	LADARCWELSAGDKWIYQAPILAAIGLNFILFLNTVRVLTATKIWETNAVGHDRKQYRK	360
Db	361	lakstlrvlvfghvlyvfcvlphsfstglgwelrhmcelfnsgfgffvsiyycngcv	420
QY	361	LAKSTLRLVLVFGVHVIVFVCLPHSFSTGLGWELRHMCELFNFSGFGFFVSIYCYNGEV	420
Db	421	qaevkkmwswrnlsvdwktptcgscrrcgsvltvthstssqsvaastrmvlisgkaak	480
QY	421	QAEVKKMWSRNWLSVDWKTPTCGSRRCGSVLTVTHTSTSSQVAAAHAWCLSLAKLPR	480
Db	481	iasrqdshltlpgyvwnssegdclphsfheet-kedsgrgddilimekpsrmpesnpt	539
QY	481	SPR-DSLTATSLYLANGVYTSQSTASHTLSTRNKEDSGRQEDDILMEKPSRMPESNPT	539
Db	540	eg 541	
QY	540	EG 541	
RESULT	2		
ENTRY	A39286	#type complete	
TITLE	parathyroid hormone / parathyroid hormone-related peptide - North American opossum		
ORGANISM	#formal_name Didelphis virginiana, Didelphis marsupialis virginiana #common_name North American opossum		
DATE	24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 30-Sep-1993		
ACCESSIONS	A39286		
REFERENCE	A39286		
#authors	Jueppner, H.; Abou-Samra, A.B.; Freeman, M.; Kong, X.F.; Schipani, E.; Richards, J.; Kolakowski Jr., L.F.; Hock, J.; Potts Jr., J.T.; Kronenberg, H.M.; Segre, G.V.		
#journal	Science (1991) 254:1024-1026		
#title	A G protein-linked receptor for parathyroid hormone and parathyroid hormone-related peptide.		
#cross-references	MUID:92054592		
#accession	A39286		
#status	preliminary; not compared with conceptual translation		
#molecule_type	mRNA		
#residues	1-585 #label JUE		
#cross-references	GB:M74445		
SUMMARY	#length 585 #molecular-weight 66007 #checksum 8339		
Query Match	49.6%; Score 2051; DB 11; Length 585;		
Best Local Similarity	55.2%; Pred. No. 0.00e+00;		
Matches	250; Conservative 106; Mismatches 87; Indels 10; Gaps 10;		
Db	102	dgcflpewdnivcwpagvgkvavpcpdyfdhnhkgrayrcdngswelvgpnrtw	161
QY	60	EGNCFPEWDLGICWPGTGVKISAVPCPPYIYDFNHKGVAFRHCPNCTWDFMSLNKT	119
Db	162	anysecvklitetr-erevf-drlgmivtgysslgsltvavilgylfrrlhtcnyl	219
QY	120	ANYSDCLRFLOPDISIGKEFCERLYVMYTVGYISFGLSVAIIIGYFRRLLHCTRNYI	179
Db	220	hmlfvsmfmravsfikdavlgygstdelel-iteelraftpppadkagfvgcrva	278
QY	180	HMHLEVSFMLRATSIKVRDVRVHAHGVKELESLIMODDPQNSIEATSVKDSQVIGCKIA	239
Db	279	vtvflyltnnywyliveglyhslilfmaffsekylgwflfvgwlpavfvavwvtvra	338
QY	240	VWMIYIFLATNYWIIWEGVLYLHNLIFVAFESTKYLIMGFILIGWGFPAAFVAAVAVARAT	299
Db	339	tlantecwdlssgnkwiqvpilaaivnvlfinilrvlatklretnagrcdtrqyr	398
QY	300	TLADARCWELSAGDKWIYQAPILAAIGLNFILFLNTVRVLTATKIWETNAVGHDRKQYR	359
Db	399	kllkstvlmlpfgvhyivfmatpevtevgilwqvgmhyemlfnsqgfavvailyfcng	458



```
Db 226 lflsflmrvsifvkdvaylsgatldaeerlteeeelralaqaqppbataaagcyrav 285
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 183 LFFVSEMLRATSIFFKDRVYVAHGVLESLIMQD-DP-QNSTEATSVKDSQYIGKIAV 240
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 286 tflyflatnywllvegylhslfmafsekylwgtvfvgwlpavfvavvsvrat 345
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 VMFIYFLATNYWILVEGLYHLNLIIFVAFSDTKYLWGFLLIGWGFPAFVAAMAVARAT 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 346 lantgwdlssgkklwllqvpllasivlnfilfinlvrvlatklretnagrcdtrgqyrk 405
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATINWETNAVGHDTKQYRK 360
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 406 llkstvlmplfgvhyvlvfmattyvsgtlwqgmhyemlfosfgffviallycfncge 465
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 361 LAKSTLVLVFGVHHYIVFVCLPHS-FTGLGWEIRMHCELFNFNSQGFVSIYYCNGE 419
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 466 vqaeinkcswrtlaifdkrkarsgssysyg-pmvshts 504
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 420 VQAEVKKMSRWLSVDWKRTPPGSRRCGSVLTTHST 459
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
ENTRY JH0594 #type complete
TITLE vasoactive intestinal peptide receptor precursor - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change
ACCESSION JH0594; S56014
REFERENCE JH0594
#authors Ishihara, T.; Shigemoto, R.; Mori, K.; Takahashi, K.; Nagata, S.
#journal Neuron (1992) 8:811-819
#title Functional expression and tissue distribution of a novel receptor for vasoactive intestinal polypeptide.
#cross-references MIM:92232309
#accession JH0594
#molecule_type mRNA
#residues 1-459 #label ISH
#cross-references GB:M6835
#experimental_source lung
#feature S56014
#authors Pei, L.; Melmed, S.
#journal Biochem. J. (1995) 308:719-723
#title Characterization of the rat vasoactive intestinal polypeptide receptor gene 5' region.
#accession S56014
#status preliminary
#molecule_type DNA
#residues 1-26 #label PEI
#cross-references EMBL:U010635
#note the translation of the nucleotide sequence is not given
KEYWORDS glycoprotein; transmembrane protein
FEATURE
1-30 #domain signal sequence #status predicted #label sig\
31-459 #product vasoactive intestinal polypeptide receptor
#status predicted #label MAR\
146-168 #domain transmembrane #label TM1\
176-195 #domain transmembrane #label TM2\
218-241 #domain transmembrane #label TM3\
256-277 #domain transmembrane #label TM4\
295-318 #domain transmembrane #label TM5\
344-363 #domain transmembrane #label TM6\
376-395 #domain transmembrane #label TM7\
58,69,100,292 #binding_site carbohydrate (Asn) (covalent) #status predicted
SUMMARY #length 459 #molecular-weight 52057 #checksum 2598
Query Match 24.88; Score 1026; DB 12; Length 459;
Best Local Similarity 40.18; Pred. No. 1.30e-150;
Matches 177; Conservative 94; Mismatches 126; Indels 44; Gaps 30;
Db 8 hvr-wicvlagalacalrpsagsaqpheceylqlieqrqc-le-eaqlenettgcs 64
```

```
QY 9 HWGWL-MIGSCLL-ARAQLSDSGITTEE-QIV-LVLKAKVQCELNITAQIQEGEGNCF 64
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 65 kmwdaltcwtprgqvavldcp-lifqlfapihynlsrsteeg-ws-q-leppg-py 118
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 65 PEWDGLICPRGTGKISAVPCPPYID-FNH-KGVAF-RHCNPNGTWDFMHSLNKWTAN 121
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 119 hiacgldrassldqqqtkfntvktgtlgysslsasllvamaillslfrklhctryyl 178
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 122 YSDC-LRFQPDISIGKQ-EFCERLYVMITVGYISFSGSLAVAILIIGYFRRLHCTRNYI 179
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 179 hnhlfmsfillratavfikdmlaf-nsg-----e-i---d-hcs-ea-sv-----gckaa 219
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 180 HNHLFVSEMLRATSIFFKDRVYVAHGVLESLIMQDPPQNSIEATSVKDSQYIGKTA 239
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 220 vffgyvcymanfllvegyllytlavsfkerkyfgylllgvpsvfittvvril 279
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 240 VVMFIYFLATNYWILVEGLYHLNLIIFVAFSDTKYLWGFLLIGWGFPAFVAAMAVARA 299
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 280 yfedfgcwtiinsslwliikapillsilvnfvlficilrllvqklrppd-igkndsspy 338
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 300 TLADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATINWETNAVGHDTKQY 358
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 339 srlakstlllilpflghyvmfaffdnfka---qvkmvfelvvgsgfgfvavilcyfing 395
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 359 RLAKSTLVLVFGVHHYIVFVCLPHSFTGLGWEIRMHCELFNFNSQGFVSIYYCNG 418
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 396 evqaelrkrkwrwhlqgvlgw 416
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 419 EVQAEVKKMSRWNL-SV-DW 437
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
ENTRY JN0604 #type complete
TITLE vasoactive intestinal peptide receptor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
ACCESSION JN0604
REFERENCE JN0604
#authors Sreedharan, S.P.; Patel, D.R.; Huang, J.X.; Goetzl, E.J.
#journal Biochem. Biophys. Res. Commun. (1993) 193:546-553
#title Cloning and functional expression of a human neuroendocrine vasoactive intestinal peptide receptor.
#accession JN0604
#molecule_type mRNA
#residues 1-457 #label SRE
#cross-references GB:L13288
#note nucleotide sequence is not given
KEYWORDS glycoprotein; hormone receptor; transmembrane protein
FEATURE
135-157 #domain transmembrane #label TM1\
175-194 #domain transmembrane #label TM2\
216-240 #domain transmembrane #label TM3\
255-276 #domain transmembrane #label TM4\
293-316 #domain transmembrane #label TM5\
342-361 #domain transmembrane #label TM6\
374-393 #domain transmembrane #label TM7\
58,69,100,290 #binding_site carbohydrate (Asn) (covalent) #status predicted
SUMMARY #length 457 #molecular-weight 51547 #checksum 9283
Query Match 24.38; Score 1003; DB 12; Length 457;
Best Local Similarity 38.48; Pred. No. 1.42e-146;
Matches 170; Conservative 103; Mismatches 128; Indels 42; Gaps 28;
Db 5 splpar-wicvlag-alavalgpaggaaarlgecdyqgmievqhkcqleeaqenetig 62
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 6 ASLHWGWL-MIGSCLLARAQLSDSGIT-IEEQIVLVKAKVQCELNIT-AQLQEGEGN 62
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 cskmdnltcwpatprgqvavilacpllfksslggrnvs-rscddeg-wt--h-le-p- 115
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 63 CPPEWDGLICPRGTGKISAVPCPP-Y-IYDFNH-KGVAFRHCNPNGTWDFMHSLNKWT 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```



```
Query Match      23.8%; Score 983; DB 12; Length 495;
Best Local Similarity 40.3%; Pred. No. 4.59e-143;
Matches 182; Conservative 91; Mismatches 107; Indels 42; Gaps 27;

Db 84 qc-le-eaqlenetigskmwnltcwpatprgqvvlacplifklfssiqgrnvs-rsc 140
QY 47 QCELNITAQLQEGEGNCPEWDGLICPRGTVGKISAVPCPP-Y-IYDENH-KGVAFRHC 103
Db 141 tdeg-wt--h-le-p-gpytiaclddaaslddeqtmfgygsvktytgyglslatly 194
QY 104 NPNGTDFMHSNLKWTWYNS-DC-LRFQPDISIGKQECERLYVMYTVGYSISFGSLAV 161
Db 195 atallsfrklhctnrnylhmlfslfiraavf-----l--kdl-alf--dsge- 239
QY 162 AILLIGFRRLHCTNRNYLHMLFVSFMRATSFVKORVVHAHIGVKELESIMQDPQN 221
Db 240 s-dqcs-egs--vgckaamffqvcvmanffllveglyltyllavsfserkyfwyil 295
QY 222 SIATSVDSKQSYIGCKIAVVMFIVFLATNYWILVEGLYLHNLIFVAFSDTKYLMGFIL 281
Db 296 igwvptftmvtwrtarihfedygllrcwdtinslwlkpgiltsilvnlfcilr 355
QY 282 IGWGFPAFVAAMAVARATLAD-A--RCWELSGADIKWIYQAPTLAAGLNFILFLNTR 338
Db 356 ilklklppdirkdss-pysrlarstlllplfgvhyimfaffpdkfp---evkmvfe 411
QY 339 VLATKIWETNAVGHDTKQYRKLAISLVLVLFVGVHYIVFVCLPHSFTGLGWEIFRMC 398
Db 412 lvgsgfgvvaallycflngvqealrkrwrhlqglvwn 453
QY 399 LFFNSFGFFVSIYCYCNGEVAEVKKMSRWNL-SV-DWK 438

RESULT 11
ENTRY      S16319      #type complete
TITLE      secretin receptor - rat
ORGANISM   #formal_name Rattus norvegicus #common_name Norway rat
DATE       13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
13-Jan-1995

ACCESSIONS S16319
REFERENCE   Ishihara, T.; Nakamura, S.; Kaziro, Y.; Takahashi, T.;
#authors    Takahashi, K.; Nagata, S.
#journal    EMBO J. (1991) 10:1635-1641
#title      Molecular cloning and expression of a cDNA encoding the
#accession  secretin receptor.
#status     preliminary
#molecule_type mRNA
#residues   S16319
#cross-references EMBL:X59132
#length 449 #molecular-weight 51234 #checksum 33

Query Match      23.6%; Score 975; DB 12; Length 449;
Best Local Similarity 40.7%; Pred. No. 1.16e-141;
Matches 184; Conservative 97; Mismatches 95; Indels 32; Gaps 16;

Db 61 etasgcglwdmncspssapartvevcgpkfllmslnkngslfrnctqdg-ws--etfp 117
QY 58 EGEKNCPEWDGLICWRPTGKISAVPCPPYIDFNHK-GVAFRHCNPNGTDFMHSNL 116
Db 118 r--pdla-cgvnlnnsfnerrhayllklkmytvgyssslamllvalscsfrlhcrt 174
QY 117 KTWANSDCLRFQPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTR 176
Db 175 nyihmhlfsvflralsnfikd---a---v---lfsddvtyc-da---hk---vvc 215
QY 177 NYIHMHLFVSFMRATSFVKORVVHAHIGVKELESIMQDPQNSIEATSVDSKQYIGC 236
Db 216 klvmiffqycimanyavllveglylhtllaisffserkylqafvllgwsgpaifvalwai 275
QY 175 NYIHMHLFVSFMRATSFVKORVVHAHIGVKELESIMQDPQNSIEATSVDSKQYIGC 236

Query Match      23.3%; Score 964; DB 14; Length 440;
Best Local Similarity 42.5%; Pred. No. 9.80e-140;
Matches 157; Conservative 87; Mismatches 93; Indels 32; Gaps 16;

Db 70 wdniscwpsvpgmvevecprflmltrngslfrnctqdg-ws--etfpr--pnlac 123
QY 67 WDGLICWRPTGKISAVPCPPYIDF-NHKGVAFRHCNPNGTDFMHSNLKWTWYNSDC 125
Db 124 avnvndssnekrhsylkikmytvgyssslvmlvalgilcafrlhcrtnyihmhlfv 183
QY 126 LRFQPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYIHMHLFV 185
Db 184 sflralsnfikd---a---v---lfsddvtyc-da---hra---gcklvmvlfqy 224
QY 186 SFMLRATSFVKORVVHAHIGVKELESIMQDPQNSIEATSVDSKQYIGCKIAVVMFY 245
Db 225 clmanyswllveglylhtllaisffserkylqafvsgpaifvalwaiarhlfedvg 284
QY 246 FLATNYWILVEGLYLHNLIFVAFSDTKYLMGFILIGWGFPAFVAAMAVARATLADAR 305
Db 285 cwdinasaiwairgvpvilsilnifilnirklrtqetgrnevs-hykrars 343
QY 306 CWELSA-GDIKWIYQAPILAAIGLNFILFLNTRVTLATKIWETNAVGHDTKQYRLAKS 364
Db 344 tlllplfgthyivfa-fspe-dam--eiqlffellalafsgqlvavlycflngevqlv 399
QY 365 TLVLVLVFGVHYIVFVCLPHSFTGLGWEIFRMCLEFNSFQGFVSIYCYCNGEVAEV 424
Db 400 qkkwqgwhl 408
QY 425 KMWMSRWNL 433

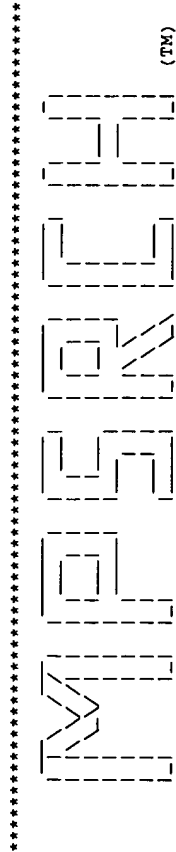
RESULT 13
ENTRY      JU0185      #type complete
TITLE      PACAP receptor subtype 3 - mouse
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change
23-Mar-1995

ACCESSIONS JU0185
```

Db	95	dg-ws---etfpd-fid-a-c-gyndpe-deskitfylvkaiytlgsvslmslttgsii	146
QY	106	NGTWDFMHSLSNKWANYSDCLRFQPDISIGKQECFERLYVMYTVGYSIFSGSLAVAIL	165
Db	147	iclfkrkhtcrnyihnlflsfmlraislvykdslysssgt--lrc---hdqp-----	195
QY	166	IGYFRRUHCCTRNTHHFLVFSFMRATSFVKDRVVHAHIGKVELSLIMQDDPQNSIEA	225
Db	196	-g---s-wvgckislvyfqcymantfyllveglyihltl-vailppscrfaylligwg	249
QY	226	TSVDKSOYGICKAVVMFIYFLATNYWILVEGLYLHNLIFVAFFSDTYLWGFILIGWG	285
Db	250	ipsvcigawiatrlslsdgwdtndhsipwwirmpillsivvnfalvisivrilqlk	309
QY	286	FPAFVAAMAVARATLADARCWELSGADIKW-IYQAPILAAAGLNFILNTVVRVLATKI	344
Db	310	-tspdvggndqsgykrklakstlllplfghvmvfaafpigiss-tyql-lf-elcvgsf	365
QY	345	WETNAVGHDRTKQYRKRLAKSTLLVLVDFGVHYIFVCLPFSHTGLGWEIRMHCELFNSF	404
Db	366	qgiwvavlycflnsevgcelkrw	389
QY	405	QGFFVSIYCYCNGEVAQVKMW	428
RESULT	15		
ENTRY	JC2463	#type complete	
TITLE	vasoactive intestinal peptide receptor - human		
ORGANISM	#formal_name Homo sapiens #common_name man		
DATE	21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 05-Jan-1996		
ACCESSIONS	JC2463		
REFERENCE	JC2463		
#authors	Svoboda, M.; Tastenoy, M.; Van Rampelbergh, J.; Goossens, J.F.; De Neef, P.; Waelbroeck, M.; Robberecht, P.		
#journal	Biochem. Biophys. Res. Commun. (1994) 205:1617-1624		
#title	Molecular cloning and functional characterization of a human VIP receptor from SUP-T1 lymphoblasts.		
#accession	JC2463		
#molecule_type	mRNA		
#residues	1-438 #label SVO		
#cross_references	GB:L36566		
#experimental_source	SUP-T1 lymphoblast cell line		
KEYWORDS	glycoprotein; receptor; transmembrane protein		
FEATURE			
	130-150	#domain transmembrane #status predicted #label TM1\	
	160-179	#domain transmembrane #status predicted #label TM2\	
	206-228	#domain transmembrane #status predicted #label TM3\	
	241-262	#domain transmembrane #status predicted #label TM4\	
	282-304	#domain transmembrane #status predicted #label TM5\	
	329-349	#domain transmembrane #status predicted #label TM6\	
	361-384	#domain transmembrane #status predicted #label TM7\	
	58,88,92	#binding_site carbohydrate (Asn) (covalent) #status predicted	
SUMMARY	#length 438 #molecular_weight 49503 #checksum 8054		
Query Match	21.2%	Score 877; DB 12; Length 438;	
Best Local Similarity	36.3%;	Pred. No. 1.56e-124;	
Matches	153; Conservative 111; Mismatches 121; Indels 36; Gaps		
Db	4	llpalltclwlapvnsipcefrhliegeetkctel-lrsg-tekhkacagvwdnic	61
QY	15	MLGSCLLARQLSDGTITIEBOIVL-VLKAKVQC-ELNITAQLOGEGNCPEPMDGLIC	72
Db	62	wrpanvgetvpcpkvfnsfyskagnisknctsdg-ws--etfpd-fvd-a-c-gysdp	114
QY	73	WPRGTGKISAVPCPPYIVDFNHKGVAE-RHCNPNGTWFHMSLNKWTWANSYDCLRFLOP	131
Db	115	e-deskitfylvkaiytlgsvslmsltagslilcflrklhtcrnyihnlflsfilra	173
QY	132	DISIGKQECFERLYVMYTVGYSIFSGSLAVAILIGYFRRLACTRNYIIMHFLVFSFMLRA	191







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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Thu Feb 6 12:25:21 1997; MasPar time 17.41 Seconds  
Tabular output not generated. 575.852 Million cell updates/sec

>US-08-468-011-2  
(1-541) from US08468011.pep  
Perfect Score: 4132  
Sequence: 1 MAWLGSALHYVWGWLMLGSL.....DDLMEKPSRPMSNPDTG 541

Scoring table: PAM 150  
Gap 11

Searched: 52205 seqs, 18531385 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot33  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10

Statistics: Mean 50.887; Variance 95.964; scale 0.530

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	3721	90.1	550	7	PTR2_HUMAN PARATHYROID HORMONE R	0.00e+00
2	2057	49.8	585	7	PTRR_DIDMA PARATHYROID HORMONE/P	0.00e+00
3	1966	47.6	591	7	PTRR_RAT PARATHYROID HORMONE/P	0.00e+00
4	1943	47.0	591	7	PTRR_MOUSE PARATHYROID HORMONE/P	0.00e+00
5	1942	47.0	593	7	PTRR_HUMAN PARATHYROID HORMONE/P	0.00e+00
6	1026	24.8	459	9	VIPR_RAT VASOACTIVE INTESTINAL	9.02e-188
7	1003	24.3	457	9	VIPR_HUMAN VASOACTIVE INTESTINAL	9.92e-183
8	975	23.6	449	8	SCRC_RAT SECRETIN RECEPTOR PRE	1.34e-176
9	964	22.3	440	8	SCRC_HUMAN SECRETIN RECEPTOR PRE	3.40e-174
10	907	22.0	437	9	VIPS_MOUSE VASOACTIVE INTESTINAL	9.38e-162
11	900	21.8	437	9	VIPS_RAT VASOACTIVE INTESTINAL	3.14e-160
12	877	21.2	438	9	VIPS_HUMAN VASOACTIVE INTESTINAL	3.18e-155
13	863	20.9	463	4	GLPR_RAT GLUCAGON-LIKE PEPTIDE	3.51e-152
14	845	20.5	477	4	GLR_HUMAN GLUCAGON RECEPTOR PRE	2.84e-148
15	845	20.5	485	4	GLR_RAT GLUCAGON RECEPTOR PRE	2.84e-148
16	828	20.0	463	4	GLPR_HUMAN GLUCAGON-LIKE PEPTIDE	1.38e-144
17	807	19.5	462	4	GIPR_HUMAN GASTRIC INHIBITORY PO	4.86e-140
18	780	18.9	468	6	PACR_HUMAN PITUITARY ADENYLATE C	3.52e-134
19	782	18.9	490	2	CALR_HUMAN CALCITONIN RECEPTOR P	1.23e-134
20	772	18.7	466	4	GIPR_HUMAN GASTRIC INHIBITORY PO	1.77e-132
21	757	18.3	423	4	GRFR_HUMAN GROWTH HORMONE-RELEAS	3.03e-129
22	753	18.2	451	4	GRFR_PIG GROWTH HORMONE-RELEAS	2.20e-128

23	754	18.2	516	2	CLRB_RAT CALCITONIN RECEPTOR B	1.34e-128
24	745	18.0	455	4	GIPR_RAT GASTRIC INHIBITORY PO	1.16e-126
25	711	17.2	423	4	GRFR_MOUSE GROWTH HORMONE-RELEAS	2.34e-119
26	704	17.0	479	2	CLRA_RAT CALCITONIN RECEPTOR A	7.42e-118
27	653	15.8	444	2	CRFR_HUMAN CORTICOTROPIN RELEASI	5.88e-107
28	653	15.8	482	2	CALR_PIG CALCITONIN RECEPTOR P	5.88e-107
29	591	14.3	411	2	CFR2_RAT CORTICOTROPIN RELEASI	8.43e-94
30	591	14.3	415	2	CRFR_MOUSE CORTICOTROPIN RELEASI	8.43e-94
31	589	14.3	415	2	CRFR_RAT CORTICOTROPIN RELEASI	2.23e-93
32	538	13.0	415	2	PACR_RAT PITUITARY ADENYLATE C	1.19e-82
33	449	10.9	464	4	GRFR_RAT GROWTH HORMONE-RELEAS	3.46e-64
34	350	8.5	395	3	DIHR_MANSE DIURETIC HORMONE RECE	3.49e-44
35	310	7.5	522	10	YOW3_CAEEL PROBABLE G PROTEIN-CO	2.48e-36
36	192	4.6	742	2	CD97_HUMAN LEUCOCYTE ANTIGEN CD9	1.64e-14
37	118	2.9	420	5	MLIC_XENLA MELATONIN RECEPTOR TY	7.29e-03
38	119	2.9	428	8	SSR3_MOUSE SOMATOSTATIN RECEPTOR	5.31e-03
39	121	2.9	748	5	JSB1_TRINI BASIC JUVENILE HORMON	2.81e-03
40	112	2.7	384	6	NK2R_BOVIN SUBSTANCE-K RECEPTOR	4.69e-02
41	107	2.6	154	9	VG51_HSVI1 HYPOTHETICAL GENE 51	2.10e-01
42	106	2.6	498	1	ADT_RICPR ADP,ATP CARRIER PROTE	2.81e-01
43	105	2.5	328	10	YHJD_ERWCH HYPOTHETICAL 36.0 KD	3.76e-01
44	105	2.5	393	10	YWCF_BAGSU HYPOTHETICAL 43.3 KD	3.76e-01
45	105	2.5	423	4	GCRC_MOUSE PROBABLE G PROTEIN-CO	3.76e-01

ALIGNMENTS

RESULT	1	PTR2_HUMAN	STANDARD;	PRT;	550 AA.
AC	P49190;				
DT	01-FEB-1996 (REL. 33, CREATED)				
DT	01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)				
DE	01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)				
DE	PARATHYROID HORMONE RECEPTOR PRECURSOR (PTH2 RECEPTOR).				
GN	PTH2.				
OS	HOMO SAPIENS (HUMAN).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; PRIMATES.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=BRAIN;				
RX	MEDLINE; 95318121.				
RA	USJN T.B., GRUBER C., BONNER T. I.;				
RL	J. BIOL. CHEM. 270:15455-15458(1995).				
CC	!- FUNCTION: THIS IS A SPECIFIC RECEPTOR FOR PARATHYROID HORMONE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL CYCLASE.				
CC	!- TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY IN BRAIN AND PANCREAS.				
CC	!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.				
DR	EMBL: U25128; G887967; -				
KW	G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.				
FT	SIGNAL	1	24		POTENTIAL.
FT	CHAIN	25	550		PARATHYROID HORMONE RECEPTOR.
FT	DOMAIN	27	145		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	146	169		1 (POTENTIAL).
FT	DOMAIN	170	176		CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	177	196		2 (POTENTIAL).
FT	DOMAIN	197	237		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	238	260		3 (POTENTIAL).
FT	DOMAIN	261	275		CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	276	297		4 (POTENTIAL).
FT	DOMAIN	298	316		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	317	337		5 (POTENTIAL).
FT	DOMAIN	338	364		CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	365	383		6 (POTENTIAL).
FT	DOMAIN	384	394		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	395	417		7 (POTENTIAL).
FT	DOMAIN	418	550		CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	51	51		POTENTIAL.
FT	CARBOHYD	106	106		POTENTIAL.
FT	CARBOHYD	116	116		POTENTIAL.
FT	CARBOHYD	121	121		POTENTIAL.
SQ	SEQUENCE	550 AA;	62235 MW;		DD481286 CRC32;







.....

DR . PIR; JN0604; JN0604.

DR . PIR; JI



[illegible]

Matches 148; Conservative 101; Mismatches 101; Indels 34; Gaps 22;

Db 37 cael-lsqm-tenracsgvwdnltcwpadgetvpcpkvfnfyrpgniskncts 94  
 QY 48 C-ELNITAOLOEGEGNCFPEWDGLICWPGTGVKISAVPCPPYIDFNHK-GVAFRHCNP 105  
 Db 95 dg-ws-etfpe-fid-a-c-gyndpe-deskifvlykaiytlgysvslmsttgsii 146  
 QY 106 NGTDFMHSLNKTNWYSDCLFLQPDISIGKQECERLYVMYTVGYSISFGSLAVAIL 165  
 Db 147 iclfrklhctryhlnflsfmralsvdkdsvlyssgl--lrc-----hdqp-----a 196  
 QY 166 IGYFRRLHCTRYIHMHLEVSFMLRATISFVKDRVHAHIGVKELESIMQDDPQNSIEA 225  
 Db 197 ----s-wgcklsivffgcymanfyllveglvhltil-vailppscflaylligw 249  
 QY 226 TSVDKSOYIGCKIAVVMYIYFLATNYIWLVEGLYHNLIFVAFSDTKYLWGFLILGW 285  
 Db 250 ipscigawtatrslsdgctndtshpwwvirmpllisivnvalfalsivrlqkl 309  
 QY 286 FPAFAVAANAVARATLADARCWELSGADIKW-IYQAPILAAIGLNFILNIVRVLATKI 344  
 Db 310 -tspdvvgndsgykrakstlllplfgvymvfaafpiss-tyqi-lf-elcvgsf 365  
 QY 345 WETNAVGHDTKQYRKRLAKSTLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNSF 404  
 Db 366 qglvvavlycflnsevccklrrw 389  
 QY 405 QGFFVSIICYNGEVAEKKMW 428

RESULT 11  
 ID VIPS RAT STANDARD; PRT; 437 AA.  
 AC P35000;  
 DT 01-FEB-1994 (REL. 28, CREATED)  
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
 DE VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 2 PRECURSOR (VIP-R-2)  
 DE (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE III RECEPTOR)  
 DE (PACAP TYPE III RECEPTOR) (PACAP-R-3).  
 OS RATTUS NORVEGICUS (RAT).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=SPRAGUE-DAWLEY; TISSUE=OLFACTORY BULB;  
 RX MEDLINE; 94039806.  
 RA LUTZ E.-M., SHEWARD W.J., WEST K.M., MORROW J.A., FINK G.,  
 RA HARMAR A.J.;  
 RA FEBS LETT. 334:3-8(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=CEREBRAL CORTEX;  
 RX MEDLINE; 95080140.  
 RA USUDIN T.B., BONNER T.I., MEZEY E.;  
 RA ENDOCRINOLOGY 135:2662-2680(1994).  
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR VIP AS WELL AS PACAP-38 AND -27,  
 CC THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH  
 CC ACTIVATE ADENYLATE CYCLASE. CAN BE COUPLED TO PHOSPHOLIPASE C.  
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.  
 DR EMBL; 225885; G414189; -;  
 DR EMBL; U09631; G495196; -;  
 DR FIR; S39069; S39069.  
 DR GCRDB; GCR\_0794; -;  
 DR PROSITE; PS00649; G-PROTEIN\_RECEP\_F2\_1.  
 DR PROSITE; PS00650; G-PROTEIN\_RECEP\_F2\_2.  
 KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.  
 FT SIGNAL 1 22 POTENTIAL.  
 FT CHAIN 23 437 VASOACTIVE INTESTINAL POLYPEPTIDE  
 FT DOMAIN 23 125 RECEPTOR 2.  
 FT TRANSMEM 126 150 EXTRACELLULAR (POTENTIAL).  
 FT 1 (POTENTIAL).

DOMAIN 151 157 CYTOPLASMIC (POTENTIAL).  
 TRANSMEM 158 177 2 (POTENTIAL).  
 DOMAIN 178 202 EXTRACELLULAR (POTENTIAL).  
 TRANSMEM 203 226 3 (POTENTIAL).  
 DOMAIN 227 239 CYTOPLASMIC (POTENTIAL).  
 TRANSMEM 240 261 4 (POTENTIAL).  
 DOMAIN 262 278 EXTRACELLULAR (POTENTIAL).  
 TRANSMEM 279 302 5 (POTENTIAL).  
 DOMAIN 303 327 CYTOPLASMIC (POTENTIAL).  
 TRANSMEM 328 347 6 (POTENTIAL).  
 DOMAIN 348 359 EXTRACELLULAR (POTENTIAL).  
 TRANSMEM 360 379 7 (POTENTIAL).  
 DOMAIN 380 437 CYTOPLASMIC (POTENTIAL).  
 CARBOHYD 57 57 POTENTIAL.  
 CARBOHYD 87 87 POTENTIAL.  
 CARBOHYD 91 91 POTENTIAL.  
 FT CONFLICT 383 383 C -> R (IN REF. 2)  
 SQ SEQUENCE 437 AA; 49552 MW; 88736A73 CRC32;

Query Match 21.8%; Score 900; DB 9; Length 437;  
 Best Local Similarity 38.0%; Pred. No. 3.14e-160;  
 Matches 146; Conservative 101; Mismatches 103; Indels 34; Gaps 22;

Db 37 cael-lsqm-enhracsgvwdnltcwpadgetvpcpkvfnfyrpgniskncts 94  
 QY 48 C-ELNITAOLOEGEGNCFPEWDGLICWPGTGVKISAVPCPPYIDFNHK-GVAFRHCNP 105  
 Db 95 dg-ws-etfpe-fid-a-c-gyndpe-deskifvlykaiytlgysvslmsttgsii 146  
 QY 106 NGTDFMHSLNKTNWYSDCLFLQPDISIGKQECERLYVMYTVGYSISFGSLAVAIL 165  
 Db 147 iclfrklhctryhlnflsfmralsvdkdsvlyssgt--lrc-----hdqp----- 195  
 QY 166 IGYFRRLHCTRYIHMHLEVSFMLRATISFVKDRVHAHIGVKELESIMQDDPQNSIEA 225  
 Db 196 -g--s-wgcklsivffgcymanfyllveglvhltil-vailppscflaylligw 249  
 QY 226 TSVDKSOYIGCKIAVVMYIYFLATNYIWLVEGLYHNLIFVAFSDTKYLWGFLILGW 285  
 Db 250 ipscigawtatrslsdgctndtshpwwvirmpllisivnvalfalsivrlqkl 309  
 QY 286 FPAFAVAANAVARATLADARCWELSGADIKW-IYQAPILAAIGLNFILNIVRVLATKI 344  
 Db 310 -tspdvvgndsgykrakstlllplfgvymvfaafpiss-tyqi-lf-elcvgsf 365  
 QY 345 WETNAVGHDTKQYRKRLAKSTLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNSF 404  
 Db 366 qglvvavlycflnsevccklrrw 389  
 QY 405 QGFFVSIICYNGEVAEKKMW 428

RESULT 12  
 ID VIPS HUMAN STANDARD; PRT; 438 AA.  
 AC P41587;  
 DT 01-NOV-1995 (REL. 32, CREATED)  
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
 DE VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 2 PRECURSOR (VIP-R-2)  
 DE (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE III RECEPTOR)  
 DE (PACAP TYPE III RECEPTOR) (PACAP-R-3) (HELODERMIN-PREFERRING VIP RECEPTOR).  
 DE VIPR2.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 95110300.  
 RA SVOBODA M., TASTENOY M., VAN RAMPENBERGH J., GOOSENS J.F., NEEF P.,  
 RA WAELEBROECK M., ROBBERECHT P.;  
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 205:1617-1624(1994).  
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR VIP AS WELL AS PACAP-38 AND -27,





Db 299 -rnsnmnyllirpalfagvnlvflrviciviaki-kanlmcktdik-cr-lakstl 354  
 QY 309 LSAGDIK-W-IYQAPILAAIGLNFLELNTVRLATKIWEINAVGHDRKQYRKLAKSTL 366  
 Db 355 tlipllgthevifafvmdhargtlrf-vkltfsltsfsgfmavlycfvnnvqmef 413  
 QY 367 VLVLVFGVHYIVFV-CLP-HSFTGLGWIRHMCLEFFNSFQGFVSIYCYCNGEVOAEV 424  
 Db 414 rkswerlwl 422  
 QY 425 KKMWSRWNL 433

RESULT 14  
 ID GLR\_HUMAN STANDARD; PRT; 477 AA.  
 AC P47871;  
 DT 01-FEB-1996 (REL. 33, CREATED)  
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
 DE GLUCAGON RECEPTOR PRECURSOR (GL-R).  
 GN GCGR. (HUMAN).  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LIVER.  
 RX MEDLINE; 94121651.  
 RA MACNEIL D.J., OCCI J.L., HEY P.J., STRADER C.D., GRAZIANO M.P.;  
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 198:328-334(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 9412999.  
 RA LOK S., KUIJPER J.L., JELINEK L.J., KRAMER J.M., WHITMORE T.E.,  
 RA SPRECHER C.A., MATHWES S., GRANT F.J., BIGGS S.H., ROSENBERG G.B.;  
 RL GENE 140:203-209(1994).  
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR GLUCAGON. THE ACTIVITY OF THIS  
 RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL  
 CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER  
 SYSTEM.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.  
 DR EMBL; U03469; G439690; -.  
 DR EMBL; L20316; G405190; -.  
 DR MIM; 138033; 11TH EDITION.  
 CC G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.  
 FT SIGNAL 1 ?  
 FT CHAIN ? 477  
 FT DOMAIN ? 142  
 FT TRANSMEM 143 166  
 FT DOMAIN 167 173  
 FT TRANSMEM 174 193  
 FT DOMAIN 194 225  
 FT TRANSMEM 226 249  
 FT DOMAIN 250 263  
 FT TRANSMEM 264 285  
 FT DOMAIN 286 303  
 FT TRANSMEM 304 326  
 FT DOMAIN 327 350  
 FT TRANSMEM 351 369  
 FT DOMAIN 370 381  
 FT TRANSMEM 382 404  
 FT DOMAIN 405 477  
 FT CARBOHYD 46 46  
 FT CARBOHYD 59 59  
 FT CARBOHYD 74 74  
 FT CARBOHYD 78 78  
 SQ SEQUENCE 477 AA; 54009 MW; DB3FF092 CRC32;

Query Match 20.5%; Score 845; DB 4; Length 477;  
 Best Local Similarity 34.4%; Pred. No. 2.84e-148;  
 Matches 137; Conservative 102; Mismatches 138; Indels 21; Gaps 17;

Db 42 qchhnlslppptelvcnrtfdkyscwpdpntantniscpwyplwhhkvqhrfvfkrcg 101  
 QY 47 QCELNITAAQLQEGEGNGCFPEWDGLICWPRCTVGKISAVPCPPYI-YDFN-HKGVAFFHCN 104  
 Db 102 pdgqw-vrgprgprwdasqc-qmdgeevqevkavkmysfgvmytvgyslslgalla 159  
 QY 105 PNGTWDPMHSLNKTWANSQCLRFLOPDISIGKQ-E-FCERLYVMVTGVYSIFGSLAVA 162  
 Db 160 lallgglskhtcrtahlanfslfklkassvldglllrrysqk-----i-gdd-l-s 211  
 QY 163 ILIIGYFRRLECHTRNYIHMLFVSMRLATSIIFVKDRVHAHIGVKLESLIMQDDPQNS 222  
 Db 212 v-stwlsdgavagrcvraavfmqygiavnycwllveglylhnllqlatlpersffslvlg 270  
 QY 223 IEATSDVKSOYIGCKIAVMFIIFLATNYWILVEGYLHNLIFVAFFSDTKLWGFILI 282  
 Db 271 gwgapmlfvvpwvavkclfcenvqwtensndmgfwllrfpflailnffivrlvqllv 330  
 QY 283 GWGPPAAFAVAVARATLADARCWELSAG-DIKWIIQAPILAAIGLNFLELNTVRLA 341  
 Db 331 akir-arqmbhtdyk-fr-lakstltlpllgvhevfvafvtdehaqgtlrsaklffdlf 387  
 QY 342 TKIWETNAVGHDRKQYRKLAKSTLVLVYGVHYIVFVCLPHSFT-GLGWETRMHCELF 400  
 Db 388 lssfgllvavlycflnkvqselrrrwhrvgkvlw 425  
 QY 401 FNSFQGFVSIYCYCNGEVOAEVKMWSRWNL-VDMW 437

RESULT 15  
 ID GLR\_RAT STANDARD; PRT; 485 AA.  
 AC P30082;  
 DT 01-APR-1993 (REL. 25, CREATED)  
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
 DE GLUCAGON RECEPTOR PRECURSOR (GL-R).  
 GN GCGR.  
 OS RATTUS NORVEGICUS (RAT).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RP [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 93206096.  
 RA JELINEK L.J., LOK S., GRANT F.J., ROSENBERG G.B., SMITH R.A.,  
 RA BENSCHE P.A., SHEPPARD P.O., O'HARA P.J., FOSTER D.C.,  
 RA KUIJPER J.L., BIGGS S.H., WALKER K.M., CHEN L.H., MCKERNAN P.A.,  
 RA KINDSVOGEL W.;  
 RA SCIENCE 259:1614-1616(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 93213282.  
 RA SVOBODA M., CICCARELLI E., TASTENOY M., CAUVIN A., STIEVENART M.,  
 RA CHRISTOPHE J.;  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-WISTAR; TISSUE=LIVER;  
 RX MEDLINE; 94364484.  
 RA MAGET B., TASTENOY M., SVOBODA M.;  
 RL FEBS LETT. 351:271-275(1994).  
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR GLUCAGON. THE ACTIVITY OF THIS  
 RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL  
 CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER  
 SYSTEM.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.  
 DR EMBL; L04796; G457614; -.  
 DR EMBL; X68692; G463258; -.  
 DR EMBL; M96674; G204374; -.  
 DR EMBL; L31574; G473766; -.  
 DR PIR; S29689; S29689.  
 DR PIR; JQ1957; JQ1957.  
 DR GCRDB; GCR\_0539; -.

DR GCRDB; GCR\_0540; -  
 DR GCRDB; GCR\_0657; -  
 DR PROSITE; PS00649; G-PROTEIN\_RECP\_F2.1.  
 DR PROSITE; PS00650; G-PROTEIN\_RECP\_F2.2.  
 KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.  
 FT SIGNAL 1 ?

FT CHAIN ? 485 GLUCAGON RECEPTOR.  
 FT DOMAIN ? 143 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 144 167 1 (POTENTIAL).  
 FT DOMAIN 168 174 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 175 194 2 (POTENTIAL).  
 FT DOMAIN 195 226 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 227 250 3 (POTENTIAL).  
 FT DOMAIN 251 264 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 265 286 4 (POTENTIAL).  
 FT DOMAIN 287 304 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 305 327 5 (POTENTIAL).  
 FT DOMAIN 328 351 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 352 370 6 (POTENTIAL).  
 FT DOMAIN 371 382 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 383 405 7 (POTENTIAL).  
 FT DOMAIN 406 485 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 47 47 POTENTIAL.  
 FT CARBOHYD 60 60 POTENTIAL.  
 FT CARBOHYD 75 75 POTENTIAL.  
 FT CARBOHYD 79 79 POTENTIAL.  
 FT CONFLICT 216 216 W -> C (IN REF. 2).  
 FT CONFLICT 324 324 V -> A (IN REF. 2).  
 SQ SEQUENCE 485 AA; 55038 MW; 05D9BFDC CRC32;

Query Match 20.5%; Score 845; DB 4; Length 485;  
 Best Local Similarity 34.0%; Pred. No. 2.84e-148;  
 Matches 133; Conservative 101; Mismatches 137; Indels 20; Gaps 15;

Db 43 qchhslslppptelvcnrtfdkyscwddtppttaniscwpypwkyhqvhrly-fkrc 101  
 QY 47 QCELNITAOQEKGNCFFPPEWGLICWPRGTGKISAVPCPPYI--YD-FNHKGVAFRHC 103  
 Db 102 gpdqgw-vrgprgqswrdasqcmdddelevqkvakmyssygmvtgyslsqallla 160  
 QY 104 NPNGTWDFMHSLNKTNWYSDC-LRFLOPDISIGKEFCERLYVMYTVGYISIFGSLAVA 162  
 Db 161 lvllglrlkhtnyihgnlfasvfkagsvllvidwllktrysqk----i-gdd-l-s 212  
 QY 163 ILIIGYERLHCTRNVIHMLFVSEMLRATSIKVRVVAHIGVKELESIMQDDPQNS 222  
 Db 213 v-svvlsgavagcrvatvmqgyianycwllvegylsllsttfseksffslylci 271  
 QY 223 IEATSVDRKSQYIGCKIAVVMFYFLATNYWILVEGLYLNLIFFVAFPSDTKYLWGFILI 282  
 Db 272 gwspllfvlpwvkvkclifenvqcvtsndmgfwllripvllailnffifvriihlv 331  
 QY 283 GWGFFPAFVAWAVARATLADARCWELSG-DIKWYQAPILAAIGLNFILNTVRVLA 341  
 Db 332 akir-ahqmhyadyk-fr-larsttilpqlgvhevfvafvtdehaqgtlrstkifdflf 388  
 QY 342 TKIWTNAGHDTKQYRKLAKSTLVLVFVGVHYIVFVCLPHSFT-GLGWEIRMHCELF 400  
 Db 389 fssfglllavlycfklnkevqaellrrwrw 419  
 QY 401 FNSFQGFVSIICNGEYQAEVKKMSRW 431

Search completed: Thu Feb 6 12:25:48 1997  
 Job time : 27 secs.

101



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 M P S R C H \_ n n  
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 (TM)  
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MPSrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm  
 Run on: Fri Feb 7 09:05:06 1997; MasPar time 1411.58 Seconds  
 Tabular output not generated. 1168.691 Million cell updates/sec

Sequence:  
 Perfect Score: 2003  
 N.A. Sequence: 1 GTTTGCTCTGGGACGCAAG.....ATTGCTGTGATTGTCA 2003  
 Comp: CAACAGAGACCGTCGGTTC.....TAACGAGACACTAACAGT

Scoring table: TABLE default  
 Gap 6

Nmatch STD : Dbase 0; Query 0  
 Searched: 279077 seqs, 411808665 bases x 2

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: emb1-new5  
 1:BCT 2:FUN 3:INV1 4:INV2 5:ORG 6:MAM 7:VRT 8:PLN 9:PRI  
 10:PRO1 11:PRO2 12:ROD 13:SYN 14:UNC 15:VIR

Database: genbank94  
 16:BCT1 17:BCT2 18:BCT3 19:BCT4 20:BCT5 21:BCT6 22:BCT7  
 23:BCT8 24:INV2 25:INV3 26:INV4 27:INV5 28:INV6 29:INV7  
 30:INV8 31:INV9 32:MAM1 33:MAM2 34:MAM3 35:VRT1 36:VRT2  
 37:VRT3 38:VRT4 39:VRT5 40:VRT6 41:VRT7 42:VRT8 43:VRT9  
 44:PLN1 45:PLN2 46:PLN3 47:PLN4 48:PLN5 49:PLN6 50:PLN7  
 51:PLN8 52:PLN9 53:PLN10 54:PLN11 55:PLN12 56:PLN13 57:PLN14  
 58:PLN15 59:PLN16 60:PLN17 61:PLN18 62:PLN19 63:PLN20  
 64:ROD1 65:ROD2 66:ROD3 67:ROD4 68:ROD5 69:ROD6 70:ROD7  
 71:ROD8 72:ROD9 73:ROD10 74:ROD11 75:ROD12 76:ROD13 77:ROD14  
 78:ROD15 79:ROD16 80:ROD17 81:ROD18

Database: genbank-news  
 82:BCT 83:INV1 84:INV2 85:MAM 86:VRT 87:PAT 88:PHG  
 89:PLN 90:PRI 91:ROD 92:STR 93:SYN 94:UNA 95:VRL  
 u-emb146\_94  
 96:part1

Statistics: Mean 11.914; Variance 4.178; scale 2.851

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1950	97.4	2641	9	Human PTH2 parathyroid	0.00e+00
2	1950	97.4	2641	56	Human PTH2 parathyroid	0.00e+00
3	626	31.3	1980	90	Human parathyroid hor	0.00e+00

ID	Score	Query Match	Length	ID	Description	Pred. No.
4	626	31.3	1980	9	Human parathyroid hor	0.00e+00
5	269	13.4	1878	33	Opossum parathyroid h	7.57e-270
6	256	12.8	2067	34	Sus scrofa parathyroi	1.86e-254
7	253	12.6	1836	69	Rat parathyroid hormo	6.53e-251
8	253	12.6	2065	69	Rat parathyroid hormo	6.53e-251
9	246	12.3	1984	64	M.musculus mRNA for p	1.21e-242
10	242	12.1	1948	60	Human parathyroid hor	6.33e-238
11	240	12.0	2095	55	H.sapiens mRNA for pa	1.44e-235
12	240	12.0	2171	56	Human parathyroid hor	1.44e-235
13	140	7.0	548	90	Human parathyroid hor	1.94e-119
14	140	7.0	548	9	Human parathyroid hor	1.94e-119
15	104	5.2	744	90	Human parathyroid hor	4.21e-79
16	104	5.2	744	9	Human parathyroid hor	4.21e-79
17	95	4.7	95	9	Human parathyroid hor	3.01e-69
18	95	4.7	95	90	Human parathyroid hor	3.01e-69
19	74	3.7	1003	55	Human parathyroid hor	8.38e-47
20	71	3.5	641	90	Human parathyroid hor	1.12e-43
21	71	3.5	641	9	Human parathyroid hor	1.12e-43
22	67	3.3	154	69	Rat parathyroid hor	1.50e-39
23	64	3.2	1766	67	Mus musculus parathyr	1.74e-36
24	61	3.0	1849	62	glucose-dependent ins	1.87e-33
25	61	3.0	2025	56	Human GIP receptor (G	1.87e-33
26	61	3.0	2181	53	H.sapiens mRNA for g1	1.87e-33
27	58	2.9	1616	56	Human secretin recept	1.86e-30
28	58	2.9	1650	56	Human secretin recept	1.86e-30
29	58	2.9	1703	56	Human secretin recept	1.86e-30
30	59	2.9	2785	63	Hamster mRNA for GIP	1.88e-31
31	57	2.8	2116	70	glucagon-like peptide	1.83e-29
32	57	2.8	3066	68	Rat mRNA sequence.	1.83e-29
33	52	2.6	2348	61	Homo sapiens vasoacti	1.41e-24
34	52	2.6	2684	56	H.sapiens HIVR mRNA f	1.41e-24
35	52	2.6	2698	68	Rattus norvegicus gss	1.41e-24
36	52	2.6	2754	61	Human vasoactive inte	1.41e-24
37	52	2.6	2834	56	H.sapiens intestinal	1.41e-24
38	50	2.5	1567	58	Human glucagon-like p	1.17e-22
39	51	2.5	1590	56	Human glucagon-like p	1.17e-22
40	51	2.5	1664	60	Human mRNA for PACAP	1.29e-23
41	51	2.5	2110	9	Human corticotropin-r	1.29e-23
42	51	2.5	2110	56	Human corticotropin-r	1.29e-23
43	50	2.5	2431	62	Human glucagon-like p	1.17e-22
44	50	2.5	3071	55	Human glucagon-like p	1.17e-22
45	49	2.4	2599	69	Rat mRNA for rat PACA	1.05e-21

## ALIGNMENTS

RESULT 1  
 ID HS251281 standard; RNA; PRI; 2641 BP.  
 AC U25128;  
 DT 08-JUL-1995 (Rel. 44, Created)  
 DE 09-APR-1996 (Rel. 47, Last updated, Version 3)  
 DE Human PTH2 parathyroid hormone receptor mRNA, complete cds.  
 KW  
 OS Homo sapiens (human)  
 OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;  
 OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Homidae.  
 RN [1]  
 RP 1-2641  
 RX MEDLINE; 95318121.  
 RA Usdin T.B., Gruber C., Bonner T.I.;  
 RT "Identification and functional expression of a receptor  
 RT selectively recognizing parathyroid hormone, the PTH2 receptor";  
 RL J. Biol. Chem. 270:15455-15458(1995).  
 RN [2]  
 RP 1-2641  
 RA Bonner T.I.;  
 RT  
 RL Submitted (17-APR-1995) to the EMBL/GenBank/DBJ databases.  
 RL Tom I. Bonner, Lab of Cell Biology, NIMH, Bldg. 36, Room 3A-17,  
 RL Bethesda, MD 20892-4090, USA  
 DR SWISS-PROT; P49190; PTR2\_HUMAN.  
 CC NCBI gi: 887966 Location/Qualifiers  
 FH key

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143..1795  
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/codon\_start=1  
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parathyroid hormone but not parathyroid hormone-related  
peptide"  
/product="PTH2 parathyroid hormone receptor"  
/db\_xref="PID:g887967"  
/db\_xref="SWISS-PROT:P49190"  
/translation="MAGLGASLHWGMLGSLARALQDSDGTFIEBQIVLVKA  
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LIIGYFRELHCTRNYIHMHLFVSPMLRATSIYFVDRVVAHIGVKELESIMQDDPON  
IEATSVKSOYIGCKIAVVMFYFLATNYWILVEGLYLHNLIFVAFSDTKYLMWGI  
IGWFPFAAFVAAMAVARATLADARCWELSDGDIKWYQAPILAAIGLNFILFLNTRV  
ATKWETNVAWGHDTRKQYRKLAKSTLVLVLFVGYHYIVFVCLPHSF7GLGWEIRHCE  
FFNSFQGFVFIYCYNGEVOAEVKMKMSRWNLSDWKRFPPCGSRRCRGSVLTVTH  
TSSQSVAAASRWVLISGKAAKIASRQPDHSITLPGYVWNSNEQDCLPHSPHEETKED  
GROGDDILMEKPSRPMESNPDETCQGETEDVL"  
polyA\_signal 2619..2625  
polyA\_site 2641  
SQ Sequence 2641 BP; 670 A; 564 C; 623 G; 784 T; 0 other;

Query Match 97.4%; Score 1950; DB 9; Length 2641;  
Best Local Similarity 99.0%; Pred. No. 0.00e+00;  
Matches 1985; Conservative 0; Mismatches 17; Indels 3; Gaps 3;

Db 53 gtttctctggccagcaagtgtgcaacttgaagcttctcccggtctctggagaggg 112  
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D 113 tccctgtcttctctacagccttcctggcagctgcctggcgggctgcctcagctc 172  
Qy 60 TCCCTGCTTCTTCTACAGCCGTTCCGGGATGGCTGGCTGGGGGGCGTGGCTCACGTC 119  
Db 173 tgggttgcttaactctggcagctgcctctggcagccagccagctgattctatgc 232  
Qy 120 TGGGGTGGCTAATGCTGGCAGCTGCCCTCTGGCCAGAGCCAGCTGGATTCTGATGC 179  
Db 233 accattactatagagagagattgtccttggcgaagcgaagcaagtaacatgaa 292  
Qy 180 ACCATCACTATAGAGAGCAGATTGCTTGTGCTGAAAGCGAAAGTACAATGTGAATC 239  
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Qy 240 AACATCACAGCTCAACTCCAGAGAGGAGAGTAATTGTTTCCCTGAAATGGGATGGACTC 299  
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Db 533 ccagatatcagtaggaaagcaagaattcttgaacgctctatgtaatgataccggt 592

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ACCESSION U25128  
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KEYWORDS human.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group;  
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Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;  
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;  
Catarrhini; Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 2641)  
AUTHORS Usdin,T.B., Gruber,C. and Bonner,T.I.  
TITLE Identification and functional expression of a receptor selectively  
recognizing parathyroid hormone, the PTH2 receptor  
J. Biol. Chem. 270 (26), 15455-15458 (1995)  
JOURNAL 95318121  
MEDLINE 2 (bases 1 to 2641)  
REFERENCE Bonner,T.I.  
AUTHORS Direct Submission  
TITLE Submitted (17-APR-1995) Tom I. Bonner, Lab of Cell Biology, NIMH,  
Bldg. 36, Room 3A-17, Bethesda, MD 20892-4090, USA  
JOURNAL Location/Qualifiers  
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NID		g1256371	
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SOURCE		Homo sapiens	
ORGANISM		Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;	
REFERENCE		Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS		Usdin,T.B.; Gruber,C. and Bonner,T.I.	
TITLE		Identification and functional expression of a receptor selectively	
JOURNAL		recognizing parathyroid hormone, the PTH2 receptor	
MEDLINE		J. Biol. Chem. 270 (26), 15455-15458 (1995)	
REFERENCE		95318121	
AUTHORS		2 (bases 1 to 1980)	
TITLE		Usdin,T.B., Modi,W. and Bonner,T.I.	
JOURNAL		Assignment of the human PTH2 receptor gene (PTH2) to chromosome	
MEDLINE		2q33 by fluorescence in situ hybridization	
REFERENCE		Unpublished	
AUTHORS		3 (bases 1 to 1980)	
TITLE		Bonner,T.I. and Usdin,T.B.	
JOURNAL		Direct Submission	
MEDLINE		Submitted (25-JAN-1996) Tom I. Bonner, Lab of Cell Biology, NIMH,	
COMMENT		Bldg. 36, Rm 3A17, MSC 4090, Bethesda, MD 20892-4090, USA	
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LOCUS 5  
DEFINITION Opossum parathyroid hormone receptor mRNA, complete cds. 27-MAY-1992  
ACCESSION M74445  
NID g164288  
KEYWORDS G protein; parathyroid hormone receptor.  
SOURCE Didelphis virginiana kidney cDNA to mRNA.  
ORGANISM Didelphis virginiana  
REFERENCE 1 (bases 1 to 1878)  
AUTHORS Juppner,H., Abou-Samra,A.-B.B., Freeman,M.W., Kong,X.F., Schipani,E., Richards,J., Kolakowski,L.F., Jr., Hock,J., Potts,J.T., Kronenberg,H.M. and Segre,G.  
TITLE A G-protein linked receptor for parathyroid hormone related peptide  
JOURNAL Science 254, 1024-1026 (1991)  
MEDLINE 92054592  
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AUTHORS			1 (bases 1 to 2095)
TITLE			Schneider,H.
JOURNAL			Direct Submission
REMARK			Submitted (02-OCT-1992) to the EMBL/GenBank/DBJ databases. H. Schneider, Preclinical Research, Sandoz Pharma AG, Bau 386 / 322, CH- 4002 Basel, SWITZERLAND
REFERENCE			sequence revised by author (17-AUG-1993)
AUTHORS			2 (bases 1 to 2095)
TITLE			Schneider,H., Feyen,J.H., Seuwen,K. and Movva,N.R.
JOURNAL			Cloning and functional expression of a human parathyroid hormone receptor
MEDLINE			Eur. J. Pharmacol. 246 (2), 149-155 (1993)
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DEFINITION Human parathyroid hormone/parathyroid hormone-related peptide  
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ACCESSION U17418

NID 9596129

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryotae; Mitochondria; Eukaryote crown group; Metazoa/Eumycota  
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Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcophylli;  
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Primates; Catarrhini; Hominoidea; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2171)

AUTHORS Levine, M.A.

TITLE Characterization of cDNA and Genomic DNA encoding the human

PTH/PTHrP receptor

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2171)

AUTHORS Levine, M. A.

TITLE Direct Submission

JOURNAL Submitted (22-NOV-1994) Levine M. A., Johns Hopkins University  
School of Medicine, Medicine/Endocrine, 720 Rutland Avenue,  
Baltimore, MD 21205, USA

FEATURES

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NID	g1256369				
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AUTHORS	Usdin,T.B., Gruber,C. and Bonner,T.I.				
TITLE	Identification and functional expression of a receptor selectively recognizing parathyroid hormone, the PTHr2 receptor				
JOURNAL	J. Biol. Chem. 270 (26), 15455-15458 (1995)				
MEDLINE	95318121				
REFERENCE	2 (bases 1 to 548)				
AUTHORS	Usdin,T.B., Modi,W. and Bonner,T.I.				
TITLE	Assignment of the human PTHr2 receptor gene (PTHr2) to chromosome 2q33 by fluorescence in situ hybridization				
JOURNAL	Unpublished				
REFERENCE	3 (bases 1 to 548)				
AUTHORS	Bonner,T.I. and Usdin,T.B.				
TITLE	Direct Submission				
JOURNAL	Submitted (25-JAN-1996) Tom I. Bonner, Lab of Cell Biology, NIMH, Bldg. 36, Rm 3A17, MSC 4090, Bethesda, MD 20892-4090, USA				
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REFERENCE 1 (bases 1 to 744)
AUTHORS Usdin,T.B., Gruber,C. and Bonner,T.I.
TITLE Identification and functional expression of a receptor selectively recognizing parathyroid hormone, the PTH2 receptor
JOURNAL J. Biol. Chem. 270 (26), 15455-15458 (1995)
MEDLINE 95318121
REFERENCE 2 (bases 1 to 744)
AUTHORS Usdin,T.B., Modi,W. and Bonner,T.I.
TITLE Assignment of the human PTH2 receptor gene (PTH2R2) to chromosome 2q33 by fluorescence in situ hybridization
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 744)
AUTHORS Bonner,T.I. and Usdin,T.B.
TITLE Direct Submission
JOURNAL Submitted (02-APR-1996) Tom I. Bonner, Lab of Cell Biology, NIMH, Bldg. 36, Rm 3A17, MSC 4090, Bethesda, MD 20892-4090, USA
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